

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Kenneth Rhodes *et al.*

Serial No.: N/A

Filed: Herewith

For: *POTASSIUM CHANNEL INTERACTORS AND
USES THEREFOR*

Attorney Docket No.: MNI-070CP4

Assistant Commissioner for Patents
Box Sequence
Washington, D.C. 20231

TRANSMITTAL LETTER FOR DISKETTE CONTAINING SEQUENCE LISTING

Dear Sir:

Enclosed is a diskette which contains a computer readable form of the Sequence Listing for the patent application filed herewith. The Sequence Listing complies with the requirements of 37 C.F.R. § 1.821. The material on this diskette is identical in substance to the sequence listing appearing on pages 1-92 of the Sequence Listing which is submitted herewith, as required by 37 C.F.R. § 1.821(f). The computer readable form of the Sequence Listing contained on the enclosed diskette is understood to comply with the requirements of § 1.824(d).

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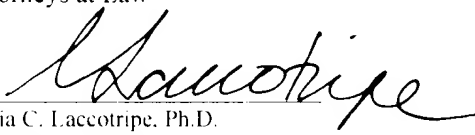
Date of Deposit September 27, 2000

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Nelson Barros
Signature

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REFERENCE LISTING

<111> Rhodes, Kenneth
Patty, Maria
Lily, Hui-Ping
An, Wenqian

<122> POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR

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 Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg
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ccc tct aaa gac aag att gag gat gag cta gag atg acc atg gtt tgc 575
 Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
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cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 623
 His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
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aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gaa tgc ctt 671
 Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
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att gtt gtt gtt att gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 719
 Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
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ttc cct cac gga gat gcc agc aca tat gaa cat tat ctg ttc aat gct 767
 Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn Ala
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210. 6

Age	Sex	Case	Notes
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[illegible]

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Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg Pro Glu
      35           40           45

Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu Leu
  50           55           60

Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val
  65           70           75           80

Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
          85           90           95

Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr Thr
      100           105           110

Gln Thr Gly Ser Val Tyr Phe Phe Arg Thr Val Thr Ala Leu Ser Ile
      115           120           125

Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu
      130           135           140

Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asn
      145           150           155

Leu Tyr Ala Arg Thr Ile Arg His Phe Val Asp Thr Phe Lys Thr Tyr
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 211 212 213

Asn Val Met
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 Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln
 1 5 10

acc aaa caa agg cga ccc tct aaa gac atc gcc tgg tgg tat tac cag 160
 Thr Lys Gln Arg Arg Pro Ser Lys Asp Ile Ala Trp Trp Tyr Tyr Gln
 15 20 25

tat cag aga gac aag att gag gat gag cta gag atg acc atg gtt tgc 208
 Tyr Gln Arg Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
 30 35 40

cac cgg cct gag gga ctg gag cag ctt gag gca cag aag aac ttc acc 256
 His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
 45 50 55 60

aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 304
 Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
 65 70 75

agg ggt ggg gtc aat gaa gaa aca ttc aag cag atc tac gat cag ttt 352
 Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
 80 85 90

ttr gtr gtr gtr tat gtr gtr gtr gtr gtr gtr gtr gtr gtr gtr gtr 400
 Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala
 95 100 105

ttc gac acc acc cag aca ggc tct gta aag ttc gag gac ttt ttr act 448
 Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Gln Asp Phe Val Thr
 110 115 120

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 Thr Thr Asn Ile Tyr Asp Ile Asn Tyr Asp Gly Tyr Thr Asn Lys Glu
 125 130 135

Lys Leu Ala Asp Val Leu Ala Met Ile Met Val Cys His Arg Phe Gln
 1 4 4

Lys Leu Ala Gln Leu Ala Ala Gln Thr Asn Phe Thr Lys Arg Gln Leu
 1 4 4

Gln Val Leu Tyr Arg Gly Ile Lys Asn Gln Cys Pro Ser Gly Val Val
 6 7 7 40

Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
 85 90 95

Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr Thr
 100 105 110

Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser Ile
 115 120 125

Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu
 130 135 140

Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asp
 145 150 155 160

Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Val
 165 170 175

Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln Lys
 180 185 190

Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu Glu
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Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe Gln
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Asn Val Met
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 sequence may be any amino acid

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20 25 30

Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
35 40 45

Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
50 55 60

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
65 70 75 80

Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln
85 90 95

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
100 105 110

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
115 120 125

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
130 135 140

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
145 150 155 160

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
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Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp
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tit gac aat gtc atc tagcccccag jagaggggggt paggggttgc tgggggggacc 1056
Phe Asp Asn Val Ile
270

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Arg Ile His Arg Pro Arg Leu Leu Asp Pro Asp Ser Val Asp Asp Glu
210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400

Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Glu Leu
410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600

Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg
610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800

Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr
1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200

Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400

Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600

Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800

Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000

Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200

Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
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Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp
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Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
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ORF 20 (1247..1247) 1247..1247

141
Cys Gly Ile Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro
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Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
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143
gag gat gag ttt gaa tta ttc aag gty tgt cac cga cat gag ggc ctg
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
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75
80

289
gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg cag gtc
Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
85
90
95

337
ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc aac gag
Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
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385
gag aac ttc aag cag att tat tct cag ttc ttt ccc caa gga gac ttc
Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
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433
agc aac tat gct act ttt ctc ttc aat gcc ttt gag acc aac cac gat
Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
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ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgc gtg att ctt
Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
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529
cgg ggg acc ata gat gat aga ctg agc tgg gct ttc aac tta tat gac
Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp
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175

577
ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac att atg
Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
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aag tc atc tat gag atg atg gac aag tac aca tac cct gct ctg cca
Lys Ser Ile Tyr Arg Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
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gag gag gcc cca aga gaa cac gtg gay agc ttc ttc cag aag atg gac
Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp
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agg ca aag gac ggc gty gty acc atc gag gaa ttc atc aac tct tct
Arg Asn Lys Ser Glu Met Met Met Met Met Met Met Met Met Met Met
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Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro
  35          40          45
Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
  50          55          60
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
  65          70          75          80
Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
          85          90          95
Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
          100          105          110
Glu Asn Phe Lys Gln Ile Tyr Ser Gln Thr Ile Phe Glu Gly Asp Ser
          115          120          125
Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
          130          135          140
Gly Ser Val Ser Pro Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
          145          150          155
Glu Asn Tyr Asp Gly Tyr Ile Thr Tyr Glu Ala Met Leu Arg Ile Met
          160          165          170

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χ^2 = 10.23, df = 1, p = .002. The significant interaction indicates that the effect of the intervention on the use of the 100% rule was significantly different for the two groups. The 100% rule was used by 100% of the control group and 80% of the intervention group.

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 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1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 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0210. 18
0211. 270
0212. PRT
0213. Mus musculus

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Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
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Phe Glu Leu Ser Thr Val Cys His Arg Leu Glu Gly Leu Glu Gln Leu
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Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg
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Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
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Age: 60y 57y 11y 71y 10y 61y 60y 60y 11y 60y 60y 60y 11y

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-210 - 19
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-212 - DNA
-213 - Homo sapiens

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- 0220·
- 0221· CDS
- 0222· (207) .. (962)

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• $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$ (one quarter of the area is shaded)

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<222> 214)..(969)

<400> 21

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agctgcctcg ccagggggcg ctgtgtgagc gccctattct ggccaccggg cgcctctctc 180

caaggccag gcgggagcgg ggccgcgggg gcc atg cgg gcc caa gcc aga aag 234
Met Arg Gly Gln Gly Arg Lys
1 5

gag agt ttg tcc gaa tcc cga gat ctg gac gcc tcc tat gac cag ctt 282
Glu Ser Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu
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acg gcc cac cct cca ggg ccc agt aaa aaa gcc ctg aag cag cgt ttc 330
Thr Gly His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe
25 30 35

ctc aag ctg ctg acg tgc tgc ggg cgc caa gcc ctg ccc tca gtc agt 378
Leu Lys Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser
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60 65 70

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85 90 95

116 Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
245 250

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Ser Val Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe
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Gln Lys Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe
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Ile Glu Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu
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Phe Asp Asn Val Ile
250

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acctgtacc tgggggtgt agggattcaa tctctgggg ctccagttagt ccagatccct 1129

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K400: 12
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 Phe Leu Phe Asn Ala Ile Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Arg Asn Leu Ser Tyr Ala Ile Asn Leu Tyr Asp Ile Asn Tyr Asn Gly
 145 150 155

His	Met	Arg	Ser	Met	Gln	Leu	Phe	Asp	Asn	Val	Ile
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1. The first group of variables includes the variables that are used to define the different types of firms. These variables are: size, age, industry, and location. The second group of variables includes the variables that are used to define the different types of financing. These variables are: type of financing, source of financing, and terms of financing. The third group of variables includes the variables that are used to define the different types of performance. These variables are: profitability, growth, and risk. The fourth group of variables includes the variables that are used to define the different types of behavior. These variables are: innovation, social responsibility, and environmental responsibility.

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 1111111111

1111111111

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
 1 5 10 15

Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Asp Asp Glu Phe Glu
 20 25 30

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 35 40 45

Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 50 55 60

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 65 70 75 80

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 85 90 95

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 100 105 110

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 115 120 125

Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 130 135 140

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 145 150 155 160

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 165 170 175

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 180 185 190

Val Val Thr Ile Phe Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
 195 200 205

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 210 215 220

1111111111
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1111111111
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.....
.....

.....
Met Arg Gly Gln Gly Arg Lys His Ser Leu Ser Asp Ser
1 5 11

aga gac ctg gac gga tcc tac gac gag ctg arg gag agc gtg gag gat 219
Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Glu Asp
15 20 25

gaa ttt gaa ttg tcc acc gtg tgt cac cgg cct gag ggt ctg gag cag 267
Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln
30 35 40 45

ctg cag gag caa acc aaa ttc acg cgc aag gag ttg cag gtc ctg tac 315
Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr
50 55 60

cgg ggc ttc aag aac gaa tgt ccg agc gga att gtc aat gag gag aac 363
Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn
65 70 75

ttc aag caa att tac tcc cag ttc ttt cct caa gga gac tcc agc acc 411
Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr
80 85 90

tat gcc act ttt ctg ttc aat gcc ttt gac acc aac cat gat ggc tgg 459
Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser
95 100 105

gtc agt ttt gag gac ttt gtg gct ggt ttg tcc gtg att ctt cgg gga 507
Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly
110 115 120 125

act gta gat gac agg ctt aat tgg gcc ttc aac ttg tat gac ctg aac 555
Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn
130 135 140

aag gac ggc tgc atc acc aac gag gaa atg ttc gac atc atg aag ttt 603
Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser
145 150 155

ata tat gac tta tta tta gac tta gaa tta tta tta tta tta gag gag 651
Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu
160 165 170

gcc cca agg gaa cat gtg gag aac ttc ttc cag aag atg gag aga aac 699
Ala Pro Arg Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn
175 180 185

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Asp His Asn Ile Met Arg Ser Met Gln Leu Ile Arg Asn Val Ile
211

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<211> 273
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Ala Thr Lys Ile Thr Arg Lys Ala Leu Ala Val Leu Tyr Arg Gly His
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Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Gln Gln Asn Phe Lys Gln
 60 65 70 75 80

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 85 90 95

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 100 105 110

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 115 120 125

Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 130 135 140

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 145 150 155 160

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 165 170 175

Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 180 185 190

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
 195 200 205

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 210 215 220

<210> 27
 <211> 2057
 <212> DNA
 <213> Simian sp.

<220>
 <221> CDS
 <222> 100% identity

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 tctctaaaga aaagccttgc cagccctcag tccgggcctc caacccagag aggtctctgt 120
 gggccagagg ggcctctgat gaggccctc tctgcctcag cccgggcctc ctcgcctcct 180

100% identity
 Leu Asp Thr Val Tyr His Asn His Ala Gly Leu Ala Gln Leu Ala Ala
 40 45

337
 His Leu Ile Lys Ile Ser Lys Lys Ala Leu Lys Val Asn Ile Leu Lys
 45 50 55

377
 Leu Leu Ile Lys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
 45 50 55

426
 agc gta gag gat gag ttt gaa tta tcc aag gtg tgt cac cga cct gag
 Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu
 60 65 70

474
 ggc ctg gaa gaa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg
 Gly Leu Glu Gln Leu Gln Gln Gln Thr Lys Phe Thr Arg Arg Glu Leu
 75 80 85

522
 cag gtc ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc
 Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
 90 95 100 105

570
 aac gag gag aac ttc aag cag att tat tct cag ttc ttt ccc caa gga
 Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
 110 115 120

618
 gac tcc agc aac tat gct act ttt ctc ttc aat gcc ttt gac acc aac
 Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn
 125 130 135

666
 cac gat ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgg gtg
 His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val
 140 145 150

714
 att ctt cgg ggg acc ata gat gat aga ctg aga tgg gct ttc aac tta
 Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu
 155 160 165

762
 tat gac ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
 170 175 180 185

810
 att atg aag tcc atc tat gac atg atg ggc aag tac aca tac cct gcc
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 190 195 200

857
 cta cgt tat atg tta cca gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 205 210 215

906
 atg gac agg aac aag gac ggc gtg gtg acc atc gag gaa ttc atc gag
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Gln Glu Phe Ile Gln
 220 225 230

954
 cta cgt tat atg tta cca gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 235 240 245

gttatgacacg ggtatgacacg ggtatgacacg ggtatgacacg 1143
 tttttttttttt tttttttttttt tttttttttttt tttttttttttt 1144
 tttttttttttt tttttttttttt tttttttttttt tttttttttttt 1145
 cgggggaaa ggggagaaa agtttggggt tggagtcagt ggttaggttt taggaattgg 1240
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 ggttcggggg cctacagccc tgggtcagca gagtatgagt tccagacatt tccagaaggt 1360
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 agtgagtcag ggatttcccg aacttgagtt ttaaccctcc tcttagtggt tgccttaggg 1660
 gaatgggaag aacccagtgt gggggcaccc attagaatct ttgcocgggt cctcacaatg 1720
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 ccagggtctg aggggaaggg cctcccggtt ccccatccgt cagacatgtt tgaatgcttt 1960
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 gctatgcaca aaaaaaaaaa aaaaaaaaaa aaaa 2057

<210> 25

<211> 252

<212> PRT

<213> Simian sp.

<410> 113

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Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45

Met Arg Gly Gln Gly Arg Lys Gln Ser Leu Ser Gln Ser Arg Asp Leu

Gln Leu Lys Leu Thr Arg Arg Gln Leu Arg Thr Leu Tyr Arg Gly Leu
 50 55

Lys Asn Glu Lys Trp Ser Gly Ile Val Asn Glu Glu Asn Ile Lys Val
100 105 110

Ile Tyr Ser Glu Phe Ile Trp Glu Gly Asp Ser Ser Asn Tyr Ala Thr
115 120 125

Phe Leu Ile Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
130 135 140

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
145 150 155 160

Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
165 170 175

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
180 185 190

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
195 200 205

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
210 215 220

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
225 230 235 240

Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
245 250

<110> 29

<111> 1904

<112> DNA

<113> Rattus sp.

<120>

<121> CDS

<222> (1)..(675)

<400> 29

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1 5 10 15

arg ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 80
Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
20 25 30

gag gat gag ttt gaa tta tcc aac gtg tct cag cga cct gag cgc ctg 144
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
35 40 45

gag ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 160
Glu Tyr Arg Gly Ile Lys Asn Glu Lys Pro Ser Gly Ile Val Asn Glu
45 50 55

[illegible]

0210 - 3C
 0211 - 225
 0212 - FET
 0213 - Fattus sp.

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0400 - 30
Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
  1              5              10              15

Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
          20              25              30

Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
          35              40              45

Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
          50              55              60

Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
  65              70              75              80

Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
          85              90              95

Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
          100              105              110

Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
          115              120              125

Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp

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1- 1- 1-
Arg Asn Lys Arg Gly Val Val Thr Ile Glu Glu Ile Ile Glu Ser Lys
175 180 185

Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ile Asp Asn Val
210 215 220

110
225

<210> 31
<211> 2841
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(768)

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gag gag ctc ggg cac aca cca ctt agc aag aag gag ggt atc aag tgg 96
Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp
20 25 30
cag agg ccg agg ctc agc cgc cag gct ttg atg aga tgc tgc ctg gtc 144
Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
35 40 45
aag tgg atc ctg tcc agc aca gcc cca cag ggc tca gat agc agc gac 192
Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp
50 55 60
agt gag ctg gag ctg tcc aag gtg cgc cac cag cca gag ggg ctg gac 240
Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
65 70 75 80
cag ctg cag gcc cag aac aag ttc aac aag aag gag ctg cag tct ctc 288
Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
85 90 95
tac agg ggc ttt aag aat gag tgt ccc aag ggc ctg gtg gac gaa gag 336
Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
100 105 110
atc ttc aaa ctc att tac gag caa ttc ttc ctc cag aga gat ttc att 384
Thr Phe Lys Leu Ile Tyr Ala Gln Phe Phe Pro Gln Gly Asp Ala Thr
115 120 125
atc att ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 432
Ala Ile His Phe Glu Asn Phe Glu Thr Glu Thr Glu Thr Glu Thr Glu Thr
130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

• •

1. 2.

42.1

672

720

768

828

888

948

1008

7068

1128

1188

1248

1393

1954

442

1438

2545

1604

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<210> 32
<211> 256
<212> PRT
<213> Homo sapiens
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<400> 32
Met Gln Pro Ala Lys Glu Val Thr Lys Ala Ser Asp Gly Ser Leu Leu
  1          5          10          15

Arg Asp Leu Gly His Thr Phe Leu Ser Lys Lys Glu Gly Ile Lys Trp
  20          25          30          35

Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
  40          45          50          55

Lys Trp Ile Leu Ser Ser Thr Ala Pro Glu Gly Ser Asp Ser Ser Arg
  60          65          70          75

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Thr Ile Tyr Leu Ile Tyr Ala Val Ile Ile Ile Val Val Tyr Asp Ala Thr
115 120 125

Thr Tyr Ala His Phe Leu Phe Asn Ala Ile Asp Ala Asp Gly Asn Gly
130 135 140

Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
145 150 155 160

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
165 170 175

Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
180 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
195 200 205

Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
210 215 220

Asn Glu Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
225 230 235 240

Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

<10> 33

<11> 442

<12> DNA

<13> Rattus sp.

<20>

<21> CDS

<22> (1)..(327)

<400> 33

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Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
1 5 10 15

cat gat ggt gtc ttt ttt ggt ttc tat tta tat gat atc aac atg gac 96
His Glu Lys Leu Lys Tyr Ala Phe Asn Ile Tyr Asp Ile Asn Lys Asp
20 25 30

ggt tac atc acc aaa gag gag atg ctg gcc atc atg aag tcc atc tac 144
Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
35 40 45

cat gat ggt gtc ttt ttt ggt ttc tat tta tat gat atc aac atg gac 192
His Glu Lys Leu Lys Tyr Ala Phe Asn Ile Tyr Asp Ile Asn Lys Asp
195 200 205

[illegible][illegible]

gaa:je'et ete tga:paau'at tette'tanta tette'geana aag'ig 442

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<210> 34
<211> 109
<212> PRT
<213> Rattus sp.
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Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
1 5 10 15

His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
20 25 30

Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
35 40 45

Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
50 55 60

Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
65 70 75 80

Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
85 90 95

Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
100 105

<210> 35
<211> 2644
<212> DNA
<213> Mus musculus

<221> CDS
<222> (49)..(816)

<400> 35

1. 2000年12月1日以前，在《中国注册会计师》杂志上公开发表过有关文章，且文章主题与注册会计师行业有关，并得到过有关方面肯定或奖励者。

arg ile arg arg arg arg arg arg arg arg arg arg arg arg arg arg arg
Arg Ile Thr Arg Gln Ala Leu Ser Arg Tyr Tyr Leu Ile Lys Thr Ile
40 45 50

arg ile arg arg arg arg arg arg arg arg arg arg arg arg arg arg arg
Leu Ser Ser Ala Ala Ile Gln Gly Ser Asp Ser Ser Asp Ser Glu Leu
55 60 65

gag tta tcc aag gta cac cat gag cca gag ggc ttg gag cag cta caa
Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp Gln Leu Gln
70 75 80

ggt cag acc aag ttc acc aag aag gag ctg cag tcc att tac cga ggc
Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu Tyr Arg Gly
85 90 95

ttc aag aat gag tgt ccc aca ggc ctg gtg gat gaa gac acc ttc aaa
Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp Thr Phe Lys
100 105 110 115

ctc att tat tcc cag ttc ttc cct cag gga gat gcc acc acc tat gca
Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr Thr Tyr Ala
120 125 130

cac ttc ctc ttc aat gcc ttt gat gct gat ggg aac ggg gcc atc cac
His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly Ala Ile His
135 140 145

ttt gag gac ttt gta gtt ggg ctc tcc atc ctg ctt cga ggg aag gtc
Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
150 155 160

cat gag aag ctc aag tgg gcc ttc aat ctc tat gac att aac aag gat
His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
165 170 175

ggt tgc atc acc aag gag gag atg ctg gcc atc atg aag tcc atc tac
Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
180 185 190 195

gac atg atg ggc cgc cac acc tac ccc atc ctg cgg gag gat cca ccc
Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
200 205 210

arg arg arg arg arg arg arg arg arg arg arg arg arg arg arg arg
Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
215 220 225

gga ctg gta acc att gat gaa ttt ctg gag act tgt cag aag gat gag
Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
230 235 240

11/1/80

11/1/80 MNI-070CP4

11/1/80

Met Val Ala Thr Lys Gln Ala Val Lys Ala Ser Asp Gly Asn Leu Leu
1 5 10 15

Gly Asp Pro Gly Arg Ile Pro Leu Ser Lys Arg Glu Ser Ile Lys Trp
20 25 30

Gln Arg Pro Arg Phe Thr Arg Gln Ala Leu Met Arg Cys Cys Leu Ile
35 40 45

Lys Trp Ile Leu Ser Ser Ala Ala Pro Gln Gly Ser Asp Ser Ser Asp
50 55 60

Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
65 70 75 80

Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
85 90 95

Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
100 105 110

Thr Phe Lys Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr
115 120 125

Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
130 135 140

Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
145 150 155 160

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
165 170 175

Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
180 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
195 200 205

Asp Ala Pro Leu Gln His Val Gln Arg Phe Phe Gln Lys Met Asp Arg
210 215 220

Asn Gln Asp Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln
225 230 235 240

Lys Asp Glu Asn Ile Met Asn Ser Met Gln Leu Phe Gln Asn Val Ile
245 250 255

11/1/80

11/1/80 MNI-070CP4

11/1/80

GenBank: U00001

GenBank:

Accession: AF011112.4, Homo sapiens

<400> 37

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Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu

20 25 30

cgg ctg atg aag ctg ttg ccc tgc tca gct gcc aaa acg tgg tct cct 144

Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro

35 40 45

gct att caa aac agc gtg gaa gat gaa ctg gag atg gcc acc gtc agg 192

Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg

50 55 60

cac cgg ccc gaa gcc ctt gag ctt ctg gaa gcc cag agc aaa ttt acc 240

His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys Phe Thr

65 70 75 80

aag aaa gag ctt cag atc ctt tac aga gga ttt aag aac gta aga act 288

Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr

85 90 95

ttc ttt ttg act tta cct tca cac aat tcc cag agg agc att gag aaa 336

Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys

100 105 110

tgagaggaaa aggggggaaaa tatcccatc tatgagaagc cccatccatc gtatatttca 396

tactgatcct tccagatag gaatataatc agtatctgtg gactttgaat ctctgtggca 456

cacccatgct ggcatactgt aattgcccat taaacaaana gtttttgaga aaaaaaaaaa 516

aaaaaaaaaa aaaaaa 531

<210> 38

<211> 112

<212> PRT

<213> Homo sapiens

<400> 38

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Gly Glu Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu

Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg

50 55 60

His Arg Phe Phe Ala Leu Ala Leu Leu Ala Ala Gln Ser Lys Phe Thr
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Lys Lys Ala Leu Ala Ile Leu Tyr Arg Gly Ile Lys Asn Val Arg Thr
 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Ile Ile Leu Thr Leu Phe Ser His Asn Ser Gln Arg Ser Ile Glu Lys
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 Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
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 Ser Met Gln Leu Phe Glu Asn Val Ile
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35 40
 41-42
 43-44
 45-46

[illegible]

Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Gln Gln Phe Ile Gln 220
 225 230

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 Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ser Pro
 235 240 245

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Leu Leu Asn
250

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cggggacaag aaagcagaaa agtcttggcc ccgagccagt ggtaggtcc taggaattgg 1243

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ccttagcaat gtcccagaaa ttccacgtac acttctcagt gtcttaggag ggcccgggat 1423

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[illegible]

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ccaggggtctg aggggaaggg cctcccggtt ccccatcgt cagacatggt tgactgcttt 1963

DECLASSIFIED BY: [redacted] DATE: 08-11-2016

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The figure is a schematic diagram of the experimental design. It shows a sequence of events in a box labeled 'Subject'. The sequence starts with 'Stimulus presentation', followed by 'Response recording', and then 'Feedback'. This sequence is repeated for multiple trials, indicated by a loop arrow. The entire process is controlled by a 'Computer' which sends signals to the 'Stimulus presentation' and 'Response recording' stages.

Met Arg Gly His Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
1 10

Asp Gly Ser Tyr Asp His Leu Thr Gly His Trp Val Gly Trp Ser Lys
20 30

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Lys Gly Pro
35 40 45

Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
50 55 60

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
65 70 75 80

Gln Thr Lys Phe Thr Arg Arg Glu Leu Glu Val Leu Tyr Arg Gly Phe
85 90 95

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
100 105 110

Ile Tyr Ser Glu Phe Phe Pro Glu Gly Asp Ser Ser Asn Tyr Ala Thr
115 120 125

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
130 135 140

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
145 150 155 160

Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
165 170 175

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
180 185 190

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
195 200 205

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
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Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
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Ile Met Arg Ser Met Gln Leu Ser Trp Leu Leu Asn
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<210> 43

<211> 26

<212> PRT

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Table 1 Description of Artificial Sequence Constructs

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Figure 1 shows a 2D hexagonal lattice. The central hexagon is labeled '1'. The six surrounding hexagons are labeled '2' through '7'. The lattice is shown in a perspective view, with the hexagons arranged in a honeycomb pattern. The labels '1' through '7' are placed inside each hexagon. The lattice is bounded by a dashed line.

A210> 50
 A211> 1591
 A212> 1134
 A213> 204440 195

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205 210 215

783
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Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys Phe Lys	1140	1160	1180	1200
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	1220	1240	1260	1280
Phe Ile Phe Gln Gly Asn Pro Tyr Phe Arg Asn Glu Gly Leu Val Lys	1300	1320	1340	1360
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	1380	1400	1420	1440
Glu Tyr Glu Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser Thr Pro	1460	1480	1500	1520
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	1540	1560	1580	1600
Ile Arg Trp His Arg Gly Gln Asp Pro Gln Ala His Ile His Arg Asn	1620	1640	1660	1680
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	1700	1720	1740	1760
Arg Glu Gly Asn Thr Ile Ile Ser Phe Phe Asn Trp Phe Ser Asp His	1780	1800	1820	1840
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	1860	1880	1900	1920
Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly Glu Leu	1940	1960	1980	2000
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	2020	2040	2060	2080
Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Met Gly Glu Gly Pro Arg Arg	2100	2120	2140	2160
aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa aaa	2180	2200	2220	2240
Asn Ile Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn	2260	2280	2300	2320

36309
 agatataaa gattatatt tttttttttt attttttttt gttttttttt aggttttttt 363
 tttttttttt attttttttt tttttttttt tttttttttt tttttttttt gttttttttt 364
 aaaaagttaa agaaaggaatg agaatgatat ttggtgattt tggaaaaggt ttatggaaag 365
 aacctgvaag atcaagggtg gggggggagg taactgagtt gctcttaagg gaagaggggg 366
 tgggggtttaa atagcaatgct tggaggaaga ttttctttaa atttttctta agtacttgaa 367
 ttcaaccagta gattttttgta aacaaaaatgt aagtcgatgt tttctctcaa ttatcttagg 368
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 ttttgcttat aattgacaac atgtgcacaaa ataccacaaat tgtgtctctgt gcaatgatgaa 371
 gaattcagtg aatattcatt aatgtattag cttgtttttg ttctctgttca tatatggctt 372
 tattctttag aataatattt gaatgtgata tttcaatagt ctgaatatatt taacaaattat 373
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 atttcttggc ctagtaatgt acttgacatt tatgttctta agcagtgtaa gtaccagtag 375
 aatttctctg tcaaaaacaaa tgaacattta gtaattttgt cttctctccat gttgttgaag 376
 gaaaaataaaa gtgtcaactac cgtattttctt gttttcacta aaaaaataaaa ataattttaa 377
 aaacaaaaaa aaaaaaaaaa 378

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<210> 55
<211> 414
<212> PRT
<213> Homo sapiens
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4100: 55
Met Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly
1 5 10
Gly Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln
15 20 25
Cys Gln Gly Leu Arg Glu Glu Thr Gln Ala Thr Gln Val Met Ala Asn
30 35 40 45
Thr Gly Gly Gly Ser Leu Gln Thr Val Ala Pro Gly Gly Ala Ser Gln
50 55 60

Ala Lys Asn Gly Lys Ala Leu Gly Ala Ile Asn Gly Ile Ala Gly Ala
111 121 131

Lys Ala Leu Ala Ala Cys Gly Ala Gly Gly Leu Gly Ser Ala Met Ile
136 146 156

Pro Gly Lys Lys Ala Lys Glu Val Thr Thr Lys Lys Arg Ala Ile Ser
145 155 165

Ala Ala Val Glu Lys Glu Gly Glu Ala Gly Ala Ala Met Glu Glu Lys
165 175

Lys Val Val Gln Lys Glu Lys Lys Val Ala Gly Gly Val Lys Glu Glu
180 185 190

Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
195 205 215

Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
210 215 220

Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
225 235 240

Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr
245 250 255

Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp
260 265 270

Glu Asp Met Leu Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys
275 285

His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Gly Asn Pro
290 295 300

Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser
305 315 320

Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
325 335

Asp Pro Phe Ala His Ile His Arg Asn Arg Ala Gly Asn Thr Ile Ile
340 345 350

Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Glu Phe Asp Arg
355 360 365

Ile Ala Glu Ile Ile Lys Gly Glu Leu Trp Pro Asn Pro Leu Gln Tyr
370 375 380

Ala Ile Val Val Val Val Val Val Val Val Val Val Val Val Val Val Val
411 421 431 441 451 461 471 481 491 501

4111-1147
4111-1150
4111-1151 sp.

4121-
4121-1151
4122- (1111-1151)

4400-56

ctg aaa ggg gag agg ccc agg ggg gtg aac tcc acc tgg agt gac ttc	48
Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Phe	
1 5 10 15	
aac cat ggc tca gct ctg cac atc gct gcc tgg aat ctg tgc ctg ggc	96
Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly	
20 25 30	
gcc gcc aaa tgt tta ctg gag cat ggt gcc aac cca gcc ctg agg aat	144
Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn	
35 40 45	
aga aaa gga cag gta cca gcc gaa gtg gtc cca gac ccc atg gac atg	192
Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met	
50 55 60	
tcc ctt gac aag gca gag gca gcc ctg gtg gcc aag gaa ttg cgg acg	240
Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr	
65 70 75 80	
ctg cta gaa gag gct gtg cca ctg tcc tgc acc ctt cct aaa gtc aca	288
Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr	
85 90 95	
cta ccc aac tat gac aac gtc cca gcc aat ctc atg ctc agc gcc ctg	336
Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu	
100 105 110	
ggc ctg cgt cta gga gac cga gtg ctc ctc gat gcc cag aag acg gcc	384
Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly	
115 120 125	
agg ctg agg ttc tgg ggg aac acc gag ttc gcc agt ggc cag tgg gta	432
Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val	
130 135 140	
ggc gtg gag cta gat gaa ccg gaa ggc aag aac gac ggc agt gtt ggt	480
Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly Ser Val Gly	
145 150 155 160	
gtt gtc agg tac ttc atc ttc cct ccc aag cag ggt ctc ttt gaa tct	528
Gly Val Arg Tyr Phe Ile Cys Ile Ile Lys Gln Gly Leu Phe Ala Ser	
165 170 175	
ctg acc ccc acc acc acc acc acc acc acc acc acc acc acc acc acc	576
Ser Thr Ile Arg Thr Ile Arg Met Asp Phe Ser Ala Val Thr Gly Lys	

Leu Gly Ser Leu Gln Gln Arg Gln Gly Ala Lys Ala Glu Val Gly Asp
235 236 237 238 239

Saa gto ett gtg gaa ggo sag aae agj gat tgt gag ttt ata tgg gaa 765
Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
245 250 255

gac aga ctt tgc tcc agg tta ctg gaa tgg cat tgaactggac cagcccacgg 821
Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
260 265

gcaagcatga cggctctgtg ttgggtgtcc ggtactttac ctgtgccccg aggcacgggg 881

tettttgcacc agcatctcgt atccagagga ttgggtggatc cactgatccc cctggagaca 941

gtgttggagc aaaaaaagtg catcaagtga caatgacaca gcccaaaagc accttcacaa 1001

cagtcaggac cccaaaggac attgcacacg agaactctat ctccaggtta ctctttctgt 1061

gctgggtttcc ttggatgctg agggcggaga tgcagtotta gagacctgga tacctgacac 1121

agagacagag tccctctag catctctga cacaaggaga cccagtcac cctaagatag 1181

agattccag tgacacctcc agaatagaaa ccccgttagc cagccctcga ttactgaggt 1241

ccattatta acagatctcc catgaagact cccccaaata cagacctcat gttaccccaa 1301

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gtttcttgagt taccagtggg ttagagtcct atgaatgaag acccccccca ccccggttct 1481

ctttaagcat aggtcatacc tccagaatag ccagccacat cactatcccc atgtaacatc 1541

41507771 Anat jicjij ajjja "iq uuaia:ita "artat :to to:ttatcaq 1691

[illegible]

U.S. DEPARTMENT OF COMMERCE

aaagtattcc tgcctctgc accttgaga aacccccagt gcttctgtatc aagccaccc 1731

SECRETARY OF THE ARMY 1541

* *****

• *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in all photosynthetic organisms. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl *a* is the most abundant pigment in most photosynthetic organisms.

gataactaat atgtgcaggg ggcaggggtt ctataggac cccaaatctt ggttctta 1381
 ctccaatctt cctttctgggtc acaggtctaa ttaataaat ctgagtcatt ggtctaaag 2441
 gaattcacag cactctgggccc agactaacag cctgagggag aacttgaggg cactctgggt 2501
 ccagagcaga cctgggggccc tgaccaccaa ggcagagctca ggaatgcctt ttaactgcct 2561
 gtccctaaac tcagcatgac tctgtctctc ttaataaag acgtttctat ggcacacaaa 2621
 aaaaaaaaaa aaaaaaaaaa aa 2643

<210> 57

<211> 267

<212> PRT

<213> Rattus sp.

<400> 57

Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Phe
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Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly
 20 25 30

Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn
 35 40 45

Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met
 50 55 60

Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr
 65 70 75 80

Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr
 85 90 95

Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu
 100 105 110

Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly
 115 120 125

Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val
 130 135 140

Val Ser Lys Val Ser Lys Ala Val Asn Ala Pro Thr Ser Ser Val Thr

Ser Thr Ser Arg Thr Ser Arg Met Asp Thr Ser Arg Val Thr Gly Lys
1 5 10

Gly Arg Arg Glu His Lys Lys Lys Lys Lys Ser Thr Ser Thr Ser Thr
15 20 25 30 35 40

Leu Gly Ser Leu Gln Gln Arg Glu Gly Ala Lys Ala Glu Val Gly Asp
45 50 55 60 65 70 75 80

Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
85 90 95 100 105 110 115 120 125

Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
125 130 135 140 145 150

<210> 58

<211> 2929

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)..(810)

<400> 58

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Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly
1 5 10 15

cgc tta gct gaa atg cct gca gat agt gga tac cct gca tac ctt ggt 96
Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly
20 25 30

gcc cga ctg gct tct ttc tat gag cga gca gcc aga gtg aaa tgt ctt 144
Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu
35 40 45

gga aac cct gag aga gaa ggg agt gtc agc att gta gga gca gtt tct 192
Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser
50 55 60

cga cct ggt ggt ggt ttt tct gat cga gtc aca tct gct act ctg ggt 240
Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly
65 70 75

att gtt cag gtg ttc tgg gcc ttg gat aag aag cta gct cag cgc aag 298
Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys
85 90 95

cac ttc cag ttc gtc aac tgg ctg att agt ttc agc aac ttc atg ggt 356
His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg
100 105 110 115 120 125

ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt 410
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
130 135 140 145 150 155 160 165 170 175 180

100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200

Mon	Tue	Wed	Thu	Fri	Sat	Sun	Mon	Tue	Wed	Thu	Fri	Sat	Sun	Mon	Tue	Wed	Thu	Fri	Sat	Sun
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
22	23	24	25	26	27	28	29	30	31	1	2	3	4	5	6	7	8	9	10	11
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	1
2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
23	24	25	26	27	28	29	30	31	1	2	3	4	5	6	7	8	9	10	11	12
13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	1	2
3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
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7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
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13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	1	2
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	1	2	3
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	1	2	3	4	5
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	1	2	3	4	5	6
18	19	20	21	22	23	24	25	26	27	28	29	30	31	1	2	3	4	5	6	7
19	20	21	22	23	24	25	26	27	28	29	30	31	1	2	3	4	5	6	7	8
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21	22	23	24	25	26	27	28	29	30	31	1	2	3	4	5	6	7	8	9	10
22	23	24	25	26	27	28	29	30	31	1	2	3	4	5	6	7	8	9	10	11
23	24	25	26	27	28	29	3													

ggg tac act cct tac gac agg ttc tgg cca atc tat aag aag gag ggg 5'c
Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
130 185 190

atg ctg tcc aac arg att tca ttc tat gat arg ggc cgg cgg gct ctg 624
Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
195 200 205

gag acc acc ggc cag agt gac aat aag atc gaa tgg tdc att atc cgt 672
Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
210 215 220

gag cac atg ggg gag att ctc tat aaa gtt tcc tct atg aaa ttc aag 120
Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys
225 230 235 240

gat cca gtg aag gat ggc gag gca aag atc aag gcc gac tac gca cag 768
Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln
245 250 255

ott ott gaa gat atg cag aac gca ttc cgt agc ctg gaa gat 810
 Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp
 250 265 270

tagaactgtg acttctctcc tctcttccg cagctcatat gtgtatatt tcttgaattt 870

ctcatctcca accctttgct tccatattgt gcagctttga gaactagtgc tegtgegttc 930

tcgttcattt tgctgtttct ttggtacgtc ttataaaaca cacattcctg tgetccgctg 990

tctgaaggag ctctgacct ttgtctgaag tgggtgaatgt agtgcatatg atacacagtg 1050

taacatacac attgtaacat ataucgttctg taaacttgta tctaaagt aa ctacccttc 1110

[illegible]

$\frac{1}{\sqrt{\pi}} \left(\frac{1}{x} + \frac{1}{y} \right) \exp \left(-\frac{1}{2} \left(\frac{1}{x} + \frac{1}{y} \right)^2 \right)$

ggtgagtaac cattttgcag gaagtatttc catttataaa acaaaagatt gatgttccaa 1290

ttatttgtag ttccccagt atcaatcag actgttttt; gctacattt taattattt 1360

[illegible]

```

tttatttat tttttatg atttttgt gttttttt ttgttttt ttgttttg 170
ctttttggc cttttgat tttttgtta tttttgaac ttgtttgt ttgttttc 180
ttttatat tttttttt ttattgttt ttatttttt ttattatat ttatttta 190
agttttcat agtttaata agacgaaga gggttttaa tttaattggc tttaaaaaa 199
aaaguaaaaa aaagtccgatt ttigtcttgc tgttttagtg tggttaata ataatcccat 1950
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aagccctgac tagtggagat gagaaagatt tcaaaaccctg tctgcctaca cctaccagca 2430
acctaggctt gtgatcagaa tgaatgatcc caagaaacta cttgaaccaag tgtgttttgt 2490
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agctccatcc tgaacaatga atagaagagg ctatataaat tgcctcotta tccttaagat 2850
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```
<210> 39
<211> 270
<212> PRT
<213> Rattus sp.
```

Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly



1. The first two lines of the code are the same as in the previous example. The third line is the same as in the previous example, but the `if` statement is used to check if the `if` statement is true. If it is true, the `if` statement is executed. If it is false, the `if` statement is not executed.

Jan. Feb. Mar. Apr. May. June. July. Aug. Sept. Oct. Nov. Dec. Jan. Feb. Mar. Apr. May. June. July. Aug. Sept. Oct. Nov. Dec.
 (b)
(c)

His His Pro Ser Val Asn Trp Leu His Ser Tyr Ser Lys Tyr Met Arg
100 100 100 100 100 100 100 100 100 100 100 100 100 100 100

Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu
115 120 125

Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu
130 135 140

Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile
 145 150 155 160

Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn
165 170 175

Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
180 185 190

Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
195 200 205

Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
210 215 220

Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys
225 230 235 240

Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln
245 250 255

Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp
260 265 270

8210. 62
 8211. 14-5
 8212. DNA
 8213. *Rattus* sp.

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<220>  
<221> CDS  
<222> (1)..(1053)  
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1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1.1) as $\epsilon \rightarrow 0$. It is shown that the solutions of the system (1.1) converge to the solutions of the system (1.2) in the sense of the weak convergence in the space $L^2(\Omega; \mathbb{R}^n)$.

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100

•

39

65

85

200

122

130

145

165

180

195

210

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1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Arar and Collins (1971) using a Shimadzu 1601 UV-Visible Spectrophotometer. The concentration of chlorophyll was expressed in mg/L.

<211> 2259

<212> DNA

<213> Simian sp.

495

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1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as $\epsilon \rightarrow 0$. It is shown that the solutions of the system (1) converge to the solutions of the system (2) in the sense of the weak convergence in the space $L^2(\Omega; \mathbb{R}^n)$.

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Ser Ser Pro Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala
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Thr Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser
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Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn
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Glu Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr
          100              105              110

Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu
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Phe Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp
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Leu Asn Tyr Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile
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Val: 1.0
Val: 1.0
Val: 1.0

04 Apr 13
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